

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

<120> SPF1-Related Transcription Factors

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<150> 60/174325

<151> 2000-01-04

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<211> 512

<212> DNA

<213> Zea mays

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 tcagattact gaagttgttt ataaaggcgtcaatcat cccaaagcccc aaccaaatag 180
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 aagaccnac cctggggggta tgactcnaat gatgtatgatg acttnggnct caaaaacgca 420
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Leu Leu Glu Arg Ser Leu Asp Gly Gln Ile Thr Glu Val Val Tyr Lys
35 40 45

Gly His His Asn His Pro Lys Pro Gln Pro Asn Arg Arg Leu Ala Ala
50 55 60

Gly Ala Val Pro Ser Ser Gln Ala Glu Glu Arg Tyr Asp Gly Val Ala
65 70 75 80

Pro Ile Glu Asp Lys Pro Ser Asn Ile Tyr Ser Asn Leu Cys Asn Gln
85 90 95

Ala His Ser Ala Gly Met Val Asp Asn Val Pro Gly Pro Ala Ser Asp
100 105 110

Asp Asp Val Asp Ala Gly Gly Arg Pro Xaa Pro Gly Gly Met Thr
115 120 125

Xaa Met Met Met Met Thr Xaa Xaa Ser Lys Thr Gln Gly Lys Trp Asn
130 135 140

Leu Pro Gly Xaa Xaa Cys Xaa Ala Leu Xaa Gly Val Asn Gln Ile Pro
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Glu Pro Xaa Xaa Pro Phe Xaa Lys Leu Phe
165 170

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 ggccgaggaa acatgttagg agccggcgcc gatcaggagc ggtctcgcc gagggggctg 240
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 gccgagctgc tcgactcgcc cgtctcgctc cactcgctt ccaacatctt ggcgtctccc 420
 accactggcg ccatcccgcc gcagaggatc gactggaaga aggccgccc cctgatcgcg 480
 tctcagtctc agcaagacgg cgacagccgg gctgcccgg ccggcttcga cgacttctcc 540
 ttcacacggg caccttcaac gccgtgcgcg cgcacacgac gacgacgtcc ttaccttcat 600
 gaagaagaan gtggagaggg ccctggccga cgggcgcatt aacgaaaaat cgngtacaaa 660
 ggcgcggcac aaacaaccon aagccggttg tncacgcgcc ggnactaa ttccgga 717

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 <211> 150
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 <213> Zea mays

<400> 4
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 20 25 30
 Asp Met Leu Gly Ala Gly Ala Asp Gln Glu Arg Ser Ser Pro Arg Gly
 35 40 45
 Leu Phe His Arg Gly Ala Arg Gly Val Pro Lys Phe Lys Ser Ala Gln
 50 55 60
 Pro Pro Ser Leu Pro Ile Ser Pro Pro Pro Met Ser Pro Ser Ser Tyr
 65 70 75 80
 Phe Ala Ile Pro Pro Gly Leu Ser Pro Ala Glu Leu Leu Asp Ser Pro
 85 90 95
 Val Leu Leu His Ser Ser Ser Asn Ile Leu Ala Ser Pro Thr Thr Gly
 100 105 110
 Ala Ile Pro Ala Gln Arg Phe Asp Trp Lys Lys Ala Ala Asp Leu Ile
 115 120 125
 Ala Ser Gln Ser Gln Gln Asp Gly Asp Ser Arg Ala Ala Ala Ala Gly
 130 135 140
 Phe Asp Asp Phe Ser Phe
 145 150

<210> 5
 <211> 1961

<212> DNA

<213> Oryza sativa

<400> 5

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gggggttggc ccaacgggttc	acgttacacgc	cgccggcggtt catcacgtcg	180
tgctgtcggg gggcggtggg	gacctgtcg	gcccggcggt tgagagcgc	240
ggttctccag aggccggagcg	agggtggcg	cgccgggtgcc caaggtaag	300
cgccgagcct gcccgtctcg	ccgcccggg	tgtcgccgtc gtcctacttc	360
cggggctcag ccccacccgag	ctgctcgact	ccccgtctc ctcagctcc	420
tggcggtcccc gaccacccgg	gcaatcccg	ctcagaggta cgactggaag	480
atctcatcgc ttctcagcaa	gatgacagcc	gccccgactt ctcctccac	540
acgcccattgc cgcgcacccg	gcctctttcc	cttccttcaa ggagcaagag	600
tcgagtcgag caagaacggc	gcccggccg	ctgtcgagcaa caagagcggc	660
acaacaagct ggaggacggg	tacaactgga	ggaagtagcg gcagaagcag	720
gcgagaaccc gaggagctac	tacaagtgc	ctacaacgg ctgtccatg	780
tggagcgttc gctcgccgac	ggccgcatc	cccagatcgt ctacaaggc	840
accccaagcc gctctccacc	gcccgaacgc	ctcttccggc tccacccggc	900
cgacgaccc tcgcccggcc	gcccggccg	cgaccagtagc tcccccggc	960
ctcctccgtc acgttccggc	acgacgaggc	cgacaacgc tcgcacccgc	1020
cgagccgaa gccaagcgt	ggaaaggagg	atgctgacaa cgagggcgc	1080
tggccggcg	cgccggcg	atgctgacaa cgagggcgc	1140
gacgatcgatcatactcgac	aacccgggtc	gcaatcccg ggtggaggaa	1200
aggcaaccc caacccaagg	agctactaca	agtgcacgc ggtggctgc	1260
agcacgtgga gccccgtcg	cacgacacgc	gccccgtgt caccacctac	1320
acaaccacga cgtccccgt	cgccggccg	gccccgtgt gacgcgc	1380
tcgcctacgg ctggggcg	tccggccg	cgacgtcg cggccccc	1440
acaccctcgatgcgttcc	aacccggcc	gctctacgg cggctacggc	1500
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tcctctgtca gtcgagccg	gcccggccg	cgactgttc gtcgagtc	1620
ccacgtggcg tatttcgccc	tcgcccgtata	gtacggccg tatacgatc	1680
tcgcacccc tgcccaacac	ggcaatacac	acatacatac tctcgatcac	1740
atacatatac agtatagttag	gtggtagtgg	tagctacta gggagtgaga	1800
tgattcgttg caggccactg	ccacgtggc	cacacggaa acagtagacg	1860
acacttggaa tacgcgtacg	tacgcacatg	tacacgttagt tttgtgcctt	1920
gagagacagg tcaaataaga	ctgatgaatt	tttcatttct t	1961

<210> 6

<211> 488

<212> PRT

<213> Oryza sativa

<400> 6

Met Ala Ser Ser Thr Gly Gly Leu Asp His Gly Phe Thr Phe Thr Pro

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Pro Pro Phe Ile Thr Ser Phe Thr Glu Leu Leu Ser Gly Gly Gly

20 25 30

Asp Leu Leu Gly Ala Gly Glu Glu Arg Ser Pro Arg Gly Phe Ser

35 40 45

Arg Gly Gly Ala Arg Val Gly Gly Gly Val Pro Lys Phe Lys Ser Ala

50 55 60

Gln Pro Pro Ser Leu Pro Leu Ser Pro Pro Pro Val Ser Pro Ser Ser

65 70 75 80

Tyr Phe Ala Ile Pro Pro Gly Leu Ser Pro Thr Glu Leu Leu Asp Ser
85 90 95

Pro Val Leu Leu Ser Ser Ser His Ile Leu Ala Phe Pro Thr Thr Gly
100 105 110

Ala Ile Pro Ala Gln Arg Tyr Asp Trp Lys Ala Ser Ala Asp Leu Ile
115 120 125

Ala Ser Gln Gln Asp Asp Ser Arg Gly Asp Phe Ser Phe His Thr Asn
130 135 140

Ser Asp Ala Met Ala Ala Gln Pro Ala Ser Phe Pro Ser Phe Lys Glu
145 150 155 160

Gln Glu Gln Gln Val Val Glu Ser Ser Lys Asn Gly Ala Ala Ala
165 170 175

Ser Ser Asn Lys Ser Gly Gly Gly Asn Asn Lys Leu Glu Asp Gly
180 185 190

Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Glu Asn
195 200 205

Pro Arg Ser Tyr Tyr Lys Cys Thr Tyr Asn Gly Cys Ser Met Lys Lys
210 215 220

Lys Val Glu Arg Ser Leu Ala Asp Gly Arg Ile Thr Gln Ile Val Tyr
225 230 235 240

Lys Gly Ala His Asn His Pro Lys Pro Leu Ser Thr Ala Ala Thr Pro
245 250 255

Leu Pro Ala Pro Pro Pro Pro Ala Pro Thr Thr Ser Arg Arg Pro
260 265 270

Ala Arg Ala Arg Thr Ser Thr Pro Pro Arg Arg Pro Arg Thr Pro Pro
275 280 285

Ser Arg Ser Ala Thr Thr Arg Pro Thr Thr His Arg Thr Ala Ala Arg
290 295 300

Ala Thr Ser Pro Lys Pro Ser Ala Gly Lys Glu Asp Ala Asp Asn Glu
305 310 315 320

Gly Ser Ser Gly Gly Met Gly Gly Ala Gly Gly Asn Pro Val Arg
325 330 335

Glu Pro Arg Leu Val Val Gln Thr Leu Ser Asp Ile Asp Ile Leu Asp
340 345 350

Asn Gly Phe Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly Asn
355 360 365

Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Val Gly Cys Pro Val
370 375 380

Arg Lys His Val Glu Arg Ala Ser His Asp Thr Arg Ala Val Ile Thr
385 390 395 400

Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Val Arg Pro Arg Arg
405 410 415

Arg Arg Arg Thr Arg Pro Gly Ala Gly Val Ala Tyr Gly Trp Gly Arg
420 425 430

Ser Gly Pro Thr Asp Val Ala Ala Ala Gln Gln Gly Pro Tyr Thr Leu
435 440 445

Glu Met Leu Pro Asn Pro Ala Gly Leu Tyr Gly Gly Tyr Gly Ala Gly
450 455 460

Ala Gly Gly Ala Ala Phe Pro Arg Thr Lys Asp Glu Arg Arg Asp Asp
465 470 475 480

Leu Phe Val Glu Ser Leu Leu Cys
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<210> 7

<211> 2086

<212> DNA

<213> Oryza sativa

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gggttggacc acgggttac 180
gttcacgccg cccgcgttca tcacgtcg 240
ctgtcggggg gcggtgggg 240
cctgctcg 240
ggggggggg aggagcg 300
ttctccagag gcgagcg 300
ggggggggc ggggtgcca agttcaagtc cgcgcagccg 360
ccgagctgc cgctctcg 360
ccgcgcgg 360
tcgcccgtcg 420
gggctcagcc 420
ccaccgagct gctgactcc 420
cccgtccccc 480
tcgcccgtc 480
ccaccgggtc aatccggct 480
cagaggtacg actgaaaggc 480
ctcatcg 540
ctcagcaaga tgacagccg 540
gycgacttct cttccacac 540
caactccgac 540
gcatggccg 600
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ctctttccct 600
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gagtcgagca 660
agaacggcgc 660
cgccgcgcg 660
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caactggagg 720
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gagaacccga 780
ggagctacta 780
caagtgcacc 780
tacaacggct 780
gctccatgaa 780
gaagaaggtg 780
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cagatcg 900
tcctccccc 900
ccgcacatcg 960
tcctccgtca 960
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ggtcgtaag 1200
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tcgacatgc 1500
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cgccgcaccaa 1560
ggacgagcgg 1560
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ggggacgacc 1560
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aaaaaaagaga 2040
gagatttttt 2040
tttaaaaaaaa 2040
aaaaaaa 2086

<210> 8
<211> 487
<212> PRT
<213> Oryza sativa

<400> 8
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Asp Leu Leu Gly Ala Gly Gly Glu Glu Arg Ser Pro Arg Gly Phe Ser
35 40 45
Arg Gly Gly Ala Arg Val Gly Gly Val Pro Lys Phe Lys Ser Ala
50 55 60
Gln Pro Pro Ser Leu Pro Leu Ser Pro Pro Pro Val Ser Pro Ser Ser
65 70 75 80
Tyr Phe Ala Ile Pro Pro Gly Leu Ser Pro Thr Glu Leu Leu Asp Ser
85 90 95
Pro Val Leu Leu Ser Ser Ser His Ile Leu Ala Ser Pro Thr Thr Gly
100 105 110
Ala Ile Pro Ala Gln Arg Tyr Asp Trp Lys Ala Ser Ala Asp Leu Ile
115 120 125
Ala Ser Gln Gln Asp Asp Ser Arg Gly Asp Phe Ser Phe His Thr Asn
130 135 140
Ser Asp Ala Met Ala Ala Gln Pro Ala Ser Phe Pro Ser Phe Lys Glu
145 150 155 160
Gln Glu Gln Gln Val Val Glu Ser Ser Lys Asn Gly Ala Ala Ala
165 170 175
Ser Ser Asn Lys Ser Gly Gly Gly Asn Asn Lys Leu Glu Asp Gly
180 185 190
Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Glu Asn
195 200 205
Pro Arg Ser Tyr Tyr Lys Cys Thr Tyr Asn Gly Cys Ser Met Lys Lys
210 215 220
Lys Val Glu Arg Ser Leu Ala Asp Gly Arg Ile Thr Gln Ile Val Tyr
225 230 235 240
Lys Gly Ala His Asn His Pro Lys Pro Leu Ser Thr Arg Arg Asn Ala
245 250 255
Ser Ser Cys Ala Thr Ala Ala Cys Ala Asp Asp Leu Ala Ala Pro
260 265 270

Gly Ala Gly Ala Asp Gln Tyr Ser Ala Ala Thr Pro Glu Asn Ser Ser
 275 280 285
 Val Thr Phe Gly Asp Asp Glu Ala Asp Asn Ala Ser His Arg Ser Glu
 290 295 300
 Gly Asp Glu Pro Glu Ala Lys Arg Trp Lys Glu Asp Ala Asp Asn Glu
 305 310 315 320
 Gly Ser Ser Gly Gly Met Gly Gly Ala Gly Gly Lys Pro Val Arg
 325 330 335
 Glu Pro Arg Leu Val Val Gln Thr Leu Ser Asp Ile Asp Ile Leu Asp
 340 345 350
 Asp Gly Phe Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly Asn
 355 360 365
 Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Val Gly Cys Pro Val
 370 375 380
 Arg Lys His Val Glu Arg Ala Ser His Asp Thr Arg Ala Val Ile Thr
 385 390 395 400
 Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Val Gly Arg Gly Gly
 405 410 415
 Gly Gly Arg Ala Pro Ala Pro Ala Pro Pro Thr Ser Gly Ala Ile
 420 425 430
 Arg Pro Ser Ala Val Ala Ala Gln Gln Gly Pro Tyr Thr Leu Glu
 435 440 445
 Met Leu Pro Asn Pro Ala Gly Leu Tyr Gly Tyr Gly Ala Gly Ala
 450 455 460
 Gly Gly Ala Ala Phe Pro Arg Thr Lys Asp Glu Arg Arg Asp Asp Leu
 465 470 475 480
 Phe Val Glu Ser Leu Leu Cys
 485

<210> 9
 <211> 1928
 <212> DNA
 <213> Glycine max

<400> 9
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 cttctccctt ggacaacaac aagccaccac agggtggttt gtctgagaga actggctctg 180
 gtgttcccaa attcaagtcc acaccaccac ttctctgtcc tctctctccc cctcccaattt 240
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 agagcttcaa ttggaagagc agttcagggg ggaatcagca aattgtcaag gaagaagaca 420
 aaagcttctc aaatttctct ttccaaatccc gatcaggacc tcctgcttca tccacagcaa 480
 cataccagtc ttcaaatgtc acagttcaaa cacaacagcc atggagttt caggaggcca 540
 cgaaacagga taatttttcc tcagggaaagg gtatgatgaa aactgaaaac tcttcttcca 600
 tgcagagttt ttccctgag attgctagtg tccaaactaa ccatagcaat gggtttcaat 660

ccgattatgg caattacccc ccacaatctc agacttaag tagaaggta gatgatgggt 720
 acaatggag gaaatatggc caaaaacaag tgaagggaaag tgaaaatcca agaagttatt 780
 acaaatgcac ataccccaat tgccctacaa agaagaagt tgagaggctc ttagatggac 840
 aaattactga gatagttat aagggtactc ataaccatcc taagcctcaa aatacttaga 900
 gaaactcatc aaactcctct tctcttgcaa tccctcattc aaattccatc agaactgaaa 960
 tcccagatca atcctatgcc acacatggaa gtggacaat ggattcagct gccacccag 1020
 aaaactcatc aatatcaatt ggagatgatg atttgagca gagttccaa aagtgtaat 1080
 caggagggaa tgaatatgat gaagatgaac ctgatgccaa aagatggaaa attgaaggtg 1140
 aaaatgaggg tatgtcagcc cctggaaagta gaacagttag agaacctaga gttgtagttc 1200
 agacaaccag tgacattgat atcctttagt atggctatag gtggagaaaa tacggcaga 1260
 aagtagtgaa gggcaatcca aatccaagga gttactacaa gtgcacacac ccaggatgtc 1320
 cagtgaggaa gcacgtggaa agagcctcac atgacctaag ggctgtgatc acaacttatg 1380
 agggaaagca caaccatgat gttcctgcag cccgtggcag tggcagccat tctgtgaaca 1440
 gaccaatgcc aaacaatgct tcaaaccaca ccaacactgc agccacttcc gtaaggctct 1500
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 aaggccaatc acccttcacc ctagagatgc tacaaagtcc aggaagttt ggattctcag 1620
 ggtttggaa tccaatgcaa tcttacgtga accagcagca actatctgac aatgtttct 1680
 cctccaggac caaggaggag cctagagatg acatgttct tgagtctcta ctatgctgaa 1740
 ggaattttt tttcccttt ttggtagcta tggaaaggttg gaaattttgg aagtggggga 1800
 ctaggattta ttggacaaat aaggtccat tcgatttatt gcatttttg gtttgggg 1860
 ttgttaaattt tatacagcca caggatttgtt atagttatata ctatgtttc aaaaaaaaaa 1920
 aaaaaaaaaa 1928

<210> 10
 <211> 575
 <212> PRT
 <213> Glycine max

<400> 10
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 Phe Thr Asn Phe Thr Phe Ser Thr His Pro Phe Met Thr Thr Ser Phe
 20 25 30
 Ser Asp Leu Leu Ala Ser Pro Leu Asp Asn Asn Lys Pro Pro Gln Gly
 35 40 45
 Gly Leu Ser Glu Arg Thr Gly Ser Gly Val Pro Lys Phe Lys Ser Thr
 50 55 60
 Pro Pro Pro Ser Leu Pro Leu Ser Pro Pro Pro Ile Ser Pro Ser Ser
 65 70 75 80
 Tyr Phe Ala Ile Pro Pro Gly Leu Ser Pro Ala Glu Leu Leu Asp Ser
 85 90 95
 Pro Val Leu Leu Asn Ser Ser Asn Ile Leu Pro Ser Pro Thr Thr Gly
 100 105 110
 Ala Phe Val Ala Gln Ser Phe Asn Trp Lys Ser Ser Ser Gly Gly Asn
 115 120 125
 Gln Gln Ile Val Lys Glu Glu Asp Lys Ser Phe Ser Asn Phe Ser Phe
 130 135 140
 Gln Thr Arg Ser Gly Pro Pro Ala Ser Ser Thr Ala Thr Tyr Gln Ser
 145 150 155 160

Ser Asn Val Thr Val Gln Thr Gln Gln Pro Trp Ser Phe Gln Glu Ala
165 170 175

Thr Lys Gln Asp Asn Phe Ser Ser Gly Lys Gly Met Met Lys Thr Glu
180 185 190

Asn Ser Ser Ser Met Gln Ser Phe Ser Pro Glu Ile Ala Ser Val Gln
195 200 205

Thr Asn His Ser Asn Gly Phe Gln Ser Asp Tyr Gly Asn Tyr Pro Pro
210 215 220

Gln Ser Gln Thr Leu Ser Arg Arg Ser Asp Asp Gly Tyr Asn Trp Arg
225 230 235 240

Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Glu Asn Pro Arg Ser Tyr
245 250 255

Tyr Lys Cys Thr Tyr Pro Asn Cys Pro Thr Lys Lys Lys Val Glu Arg
260 265 270

Ser Leu Asp Gly Gln Ile Thr Glu Ile Val Tyr Lys Gly Thr His Asn
275 280 285

His Pro Lys Pro Gln Asn Thr Arg Arg Asn Ser Ser Asn Ser Ser Ser
290 295 300

Leu Ala Ile Pro His Ser Asn Ser Ile Arg Thr Glu Ile Pro Asp Gln
305 310 315 320

Ser Tyr Ala Thr His Gly Ser Gly Gln Met Asp Ser Ala Ala Thr Pro
325 330 335

Glu Asn Ser Ser Ile Ser Ile Gly Asp Asp Asp Phe Glu Gln Ser Ser
340 345 350

Gln Lys Cys Lys Ser Gly Gly Asp Glu Tyr Asp Glu Asp Glu Pro Asp
355 360 365

Ala Lys Arg Trp Lys Ile Glu Gly Glu Asn Glu Gly Met Ser Ala Pro
370 375 380

Gly Ser Arg Thr Val Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser
385 390 395 400

Asp Ile Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln
405 410 415

Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr
420 425 430

His Pro Gly Cys Pro Val Arg Lys His Val Glu Arg Ala Ser His Asp
435 440 445

Leu Arg Ala Val Ile Thr Thr Tyr Glu Gly Lys His Asn His Asp Val
450 455 460

Pro Ala Ala Arg Gly Ser Gly Ser His Ser Val Asn Arg Pro Met Pro
465 470 475 480

Asn Asn Ala Ser Asn His Thr Asn Thr Ala Ala Thr Ser Val Arg Leu
 485 490 495

Leu Pro Val Ile His Gln Ser Asp Asn Ser Leu Gln Asn Gln Arg Ser
 500 505 510

Gln Ala Pro Pro Glu Gly Gln Ser Pro Phe Thr Leu Glu Met Leu Gln
 515 520 525

Ser Pro Gly Ser Phe Gly Phe Ser Gly Phe Gly Asn Pro Met Gln Ser
 530 535 540

Tyr Val Asn Gln Gln Leu Ser Asp Asn Val Phe Ser Ser Arg Thr
 545 550 555 560

Lys Glu Glu Pro Arg Asp Asp Met Phe Leu Glu Ser Leu Leu Cys
 565 570 575

<210> 11

<211> 2158

<212> DNA

<213> Triticum aestivum

<400> 11

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<211> 619
<212> PRT
<213> Triticum aestivum

<400> 12
Thr Ser Arg Thr Ala Pro Met Ala Asp Ser Pro Asn Pro Ser Ser Gly
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Asp Leu Pro Ser Ala Ala Gly Ser Ser Pro Glu Lys Pro Tyr Pro Ala
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Asp Arg Arg Val Ala Ala Leu Ala Gly Ala Gly Ala Arg Tyr Lys Ala
35 40 45

Met Ser Pro Ala Arg Leu Pro Ile Ser Arg Glu Pro Cys Leu Thr Ile
50 55 60

Pro Ala Gly Phe Ser Pro Ser Ala Leu Leu Asp Ser Pro Val Leu Leu
65 70 75 80

Thr Asn Phe Lys Val Glu Pro Ser Pro Thr Thr Gly Ser Leu Ser Met
85 90 95

Ala Ala Ile Met His Lys Ser Ala His Pro Asp Ile Leu Pro Ser Pro
100 105 110

Arg Asp Lys Ser Ile Arg Ala His Glu Asp Gly Gly Ser Arg Asp Phe
115 120 125

Glu Phe Lys Pro His Leu Asn Ser Ser Ser Gln Ser Leu Ala Pro Ala
130 135 140

Met Ser Asp Leu Lys Lys His Glu His Ser Met Gln Asn Gln Ser Met
145 150 155 160

Asn Pro Ser Ser Ser Ser Asn Met Val Asn Glu Asn Arg Pro Pro
165 170 175

Cys Ser Arg Glu Ser Ser Leu Thr Val Asn Val Ser Ala Pro Asn Gln
180 185 190

Pro Val Gly Met Val Gly Leu Thr Asp Asn Met Pro Ala Glu Val Gly
195 200 205

Thr Ser Glu Pro Gln Gln Met Asn Ser Ser Asp Asn Ala Met Gln Glu
210 215 220

Pro Gln Ser Glu Asn Val Ala Asp Lys Ser Ala Asp Asp Gly Tyr Asn
225 230 235 240

Trp Arg Lys Tyr Gly Gln Lys His Val Lys Gly Ser Glu Asn Pro Arg
245 250 255

Ser Tyr Tyr Lys Cys Thr His Pro Asn Cys Glu Val Lys Lys Leu Leu
260 265 270

Glu Arg Ala Val Asp Gly Leu Ile Thr Glu Val Val Tyr Lys Gly Arg
275 280 285

His Asn His Pro Lys Pro Gln Pro Asn Arg Arg Leu Ala Gly Gly Ala
290 295 300

Val Pro Ser Asn Gln Gly Glu Glu Arg Tyr Asp Gly Ala Ala Ala Ala
305 310 315 320

Asp Asp Lys Ser Ser Asn Ala Leu Ser Asn Leu Ala Asn Pro Val Asn
325 330 335

Ser Pro Gly Met Val Glu Pro Val Pro Val Ser Val Ser Asp Asp Asp
340 345 350

Ile Asp Ala Gly Gly Arg Pro Tyr Pro Gly Asp Asp Ala Thr Glu
355 360 365

Glu Asp Leu Glu Ser Lys Arg Arg Lys Met Glu Ser Ala Gly Ile Asp
370 375 380

Ala Ala Leu Met Gly Lys Pro Asn Arg Glu Pro Arg Val Val Val Gln
385 390 395 400

Thr Val Ser Glu Val Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys
405 410 415

Tyr Gly Gln Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr
420 425 430

Lys Cys Thr Ser Thr Gly Cys Pro Val Arg Lys His Val Glu Arg Ala
435 440 445

Ser His Asp Pro Lys Ser Val Ile Thr Thr Tyr Glu Gly Lys His Asn
450 455 460

His Glu Val Pro Ala Ala Arg Asn Ala Thr His Glu Met Ser Ala Pro
465 470 475 480

Pro Met Lys Asn Val Val His Gln Ile Asn Ser Ser Met Pro Ser Ser
485 490 495

Ile Gly Gly Met Met Arg Ala Cys Glu Ala Arg Asn Phe Ser Asn Gln
500 505 510

Tyr Ser Gln Ala Ala Glu Thr Asp Asn Val Ser Leu Asp Leu Gly Val
515 520 525

Gly Ile Ser Pro Asn His Ser Asp Ala Thr Asn Gln Met Gln Ser Ser
530 535 540

Gly Pro Asp Gln Met Gln Tyr Gln Met Gln Ser Met Ala Ser Met Tyr
545 550 555 560

Gly Asn Met Arg His Pro Ser Ser Met Ala Val Pro Thr Val Gln Gly
565 570 575

Asn Ser Ala Gly Arg Met Tyr Gly Ser Arg Glu Glu Lys Gly Asn Glu
580 585 590

Gly Phe Thr Phe Arg Ala Thr Pro Met Asp His Ser Ala Asn Leu Cys
595 600 605

Tyr Ser Gly Ala Gly Asn Leu Val Met Gly Pro
610 615

<210> 13
<211> 549
<212> PRT
<213> Ipomoea batatas

<400> 13
Met Ala Ala Ser Ser Gly Thr Ile Asp Ala Pro Thr Ala Ser Ser Ser
1 5 10 15

Phe Ser Phe Ser Thr Ala Ser Ser Phe Met Ser Ser Phe Thr Asp Leu
20 25 30

Leu Ala Ser Asp Ala Tyr Ser Gly Gly Ser Val Ser Arg Gly Leu Gly
35 40 45

Asp Arg Ile Ala Glu Arg Thr Gly Ser Gly Val Pro Lys Phe Lys Ser
50 55 60

Leu Pro Pro Pro Ser Leu Pro Leu Ser Ser Pro Ala Val Ser Pro Ser
65 70 75 80

Ser Tyr Phe Ala Phe Pro Pro Gly Leu Ser Pro Ser Glu Leu Leu Asp
85 90 95

Ser Pro Val Leu Leu Ser Ser Ser Asn Ile Leu Pro Ser Pro Thr Thr
100 105 110

Gly Thr Phe Pro Ala Gln Thr Phe Asn Trp Lys Asn Asp Ser Asn Ala
115 120 125

Ser Gln Glu Asp Val Lys Gln Glu Glu Lys Gly Tyr Pro Asp Phe Ser
130 135 140

Phe Gln Thr Asn Ser Ala Ser Met Thr Leu Asn Tyr Glu Asp Ser Lys
145 150 155 160

Arg Lys Asp Glu Leu Asn Ser Leu Gln Ser Leu Pro Pro Val Thr Thr
165 170 175

Ser Thr Gln Met Ser Ser Gln Asn Asn Gly Gly Ser Tyr Ser Glu Tyr
180 185 190

Asn Asn Gln Cys Cys Pro Pro Ser Gln Thr Leu Arg Glu Gln Arg Arg
195 200 205

Ser Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Gln Val Lys
210 215 220

Gly Ser Glu Asn Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro Asn Cys
225 230 235 240

Pro Thr Lys Lys Lys Val Glu Arg Ala Leu Asp Gly Gln Ile Thr Glu
245 250 255

Ile Val Tyr Lys Gly Ala His Asn His Pro Lys Pro Gln Ser Thr Arg
260 265 270

Arg Ser Ser Ser Ser Thr Ala Ser Ser Ala Ser Thr Ile Ala Ala Gln
275 280 285

Ser Tyr Asn Ala Pro Ala Ser Asp Val Pro Asp Gln Ser Tyr Trp Ser
290 295 300

Asn Gly Asn Gly Gln Met Asp Ser Val Ala Thr Pro Glu Asn Ser Ser
305 310 315 320

Ile Ser Val Gly Asp Asp Glu Phe Glu Gln Ser Ser Gln Lys Arg Glu
325 330 335

Ser Gly Gly Asp Glu Phe Asp Glu Asp Glu Pro Asp Ala Lys Arg Trp
340 345 350

Lys Val Glu Asn Glu Ser Glu Gly Val Ser Ala Gln Gly Ser Arg Thr
355 360 365

Val Arg Glu Pro Arg Val Val Gln Thr Thr Ser Asp Ile Asp Ile
370 375 380

Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys
385 390 395 400

Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ser Gln Gly Cys
405 410 415

Pro Val Arg Lys His Val Glu Arg Ala Ser His Asp Ile Arg Ser Val
420 425 430

Ile Thr Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Ala Ala Arg
435 440 445

Gly Ser Gly Ser His Gly Leu Asn Arg Gly Ala Asn Pro Asn Asn Asn
450 455 460

Ala Ala Met Ala Met Ala Ile Arg Pro Ser Thr Met Ser Leu Gln Ser
465 470 475 480

Asn Tyr Pro Ile Pro Ile Pro Ser Thr Arg Pro Met Gln Gln Gly Glu
485 490 495

Gly Gln Ala Pro Tyr Glu Met Leu Gln Gly Ser Gly Gly Phe Gly Tyr
500 505 510

Ser Gly Phe Gly Asn Pro Met Asn Ala Tyr Ala Asn Gln Ile Gln Asp
515 520 525

Asn Ala Phe Ser Arg Ala Lys Glu Glu Pro Arg Asp Asp Leu Phe Leu
530 535 540

Asp Thr Leu Leu Ala
545

<210> 14
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14
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36